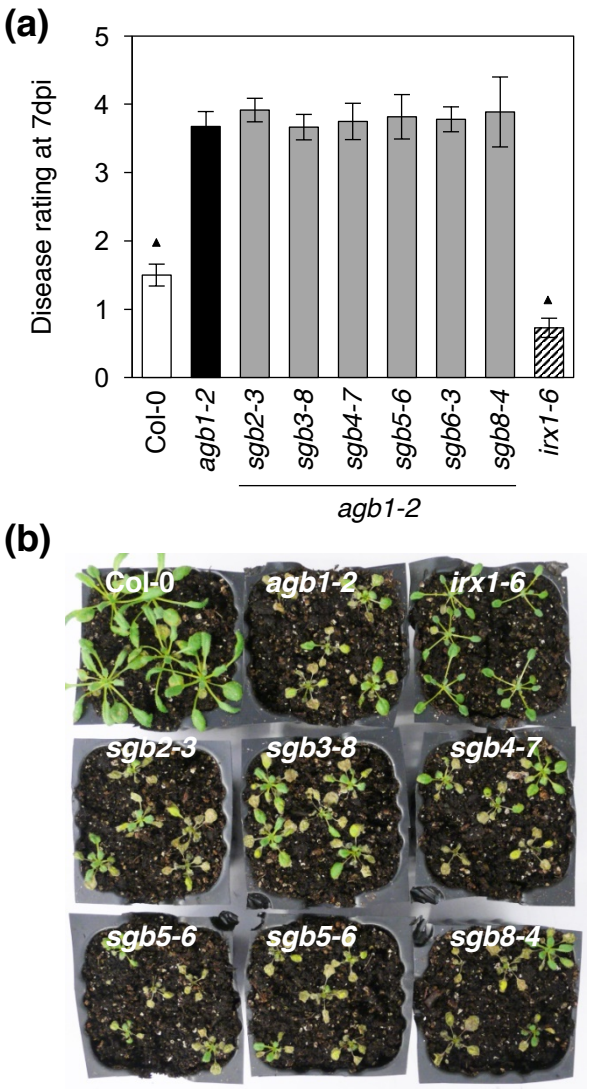


Figure S1. Susceptibility of *sgb* mutants to *PcBMM*.
(a) Average disease rating (DR ± SE) of wild type, *agb1-2* and *sgb* mutants at 7 dpi with *PcBMM*. The *irx1-6* line was included as resistance control. The DR varies between 0 (no symptoms) and 5 (dead plant). At least 15 plants per genotype were tested in each experiment. Black triangles indicate groups statistically different from *agb1-2* plants (Student's *t*-test, $p < 0.05$). This assay has been performed three times with similar results. (b) Macroscopic disease symptoms of the indicated genotypes at 7 dpi with a suspension of $4x10^6$ spores/ml of *PcBMM*.

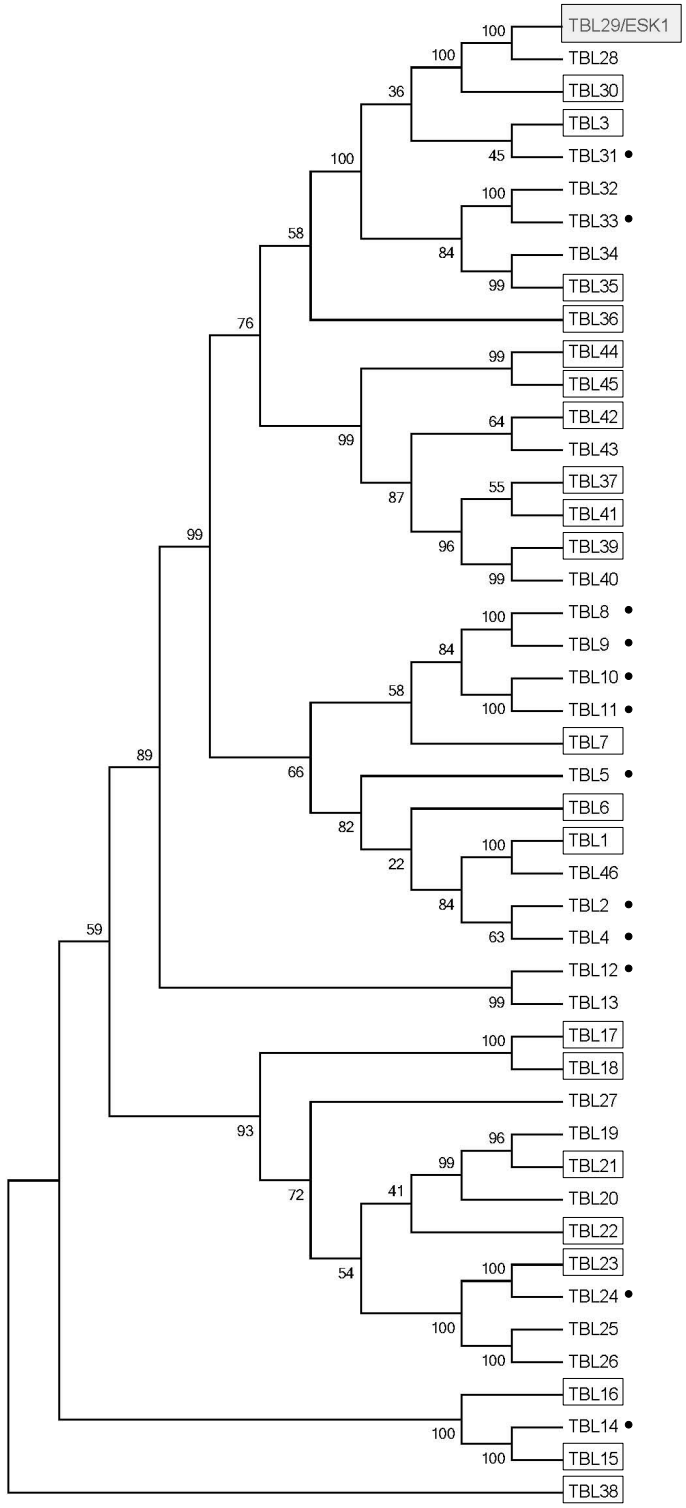


Figure S2. Arabidopsis TBL members. Phylogeny reconstruction using the Neighbor-Joining statistical method based on the protein sequence of all Arabidopsis TBL family members including ESKIMO1 protein (TBL29, in a grey box). TBL members whose expression is induced by pathogens are in boxes (based on Arabidopsis eFP Browser; Winter *et al*., 2007). Those members labelled with a dot cannot be found in ATH1 data source.

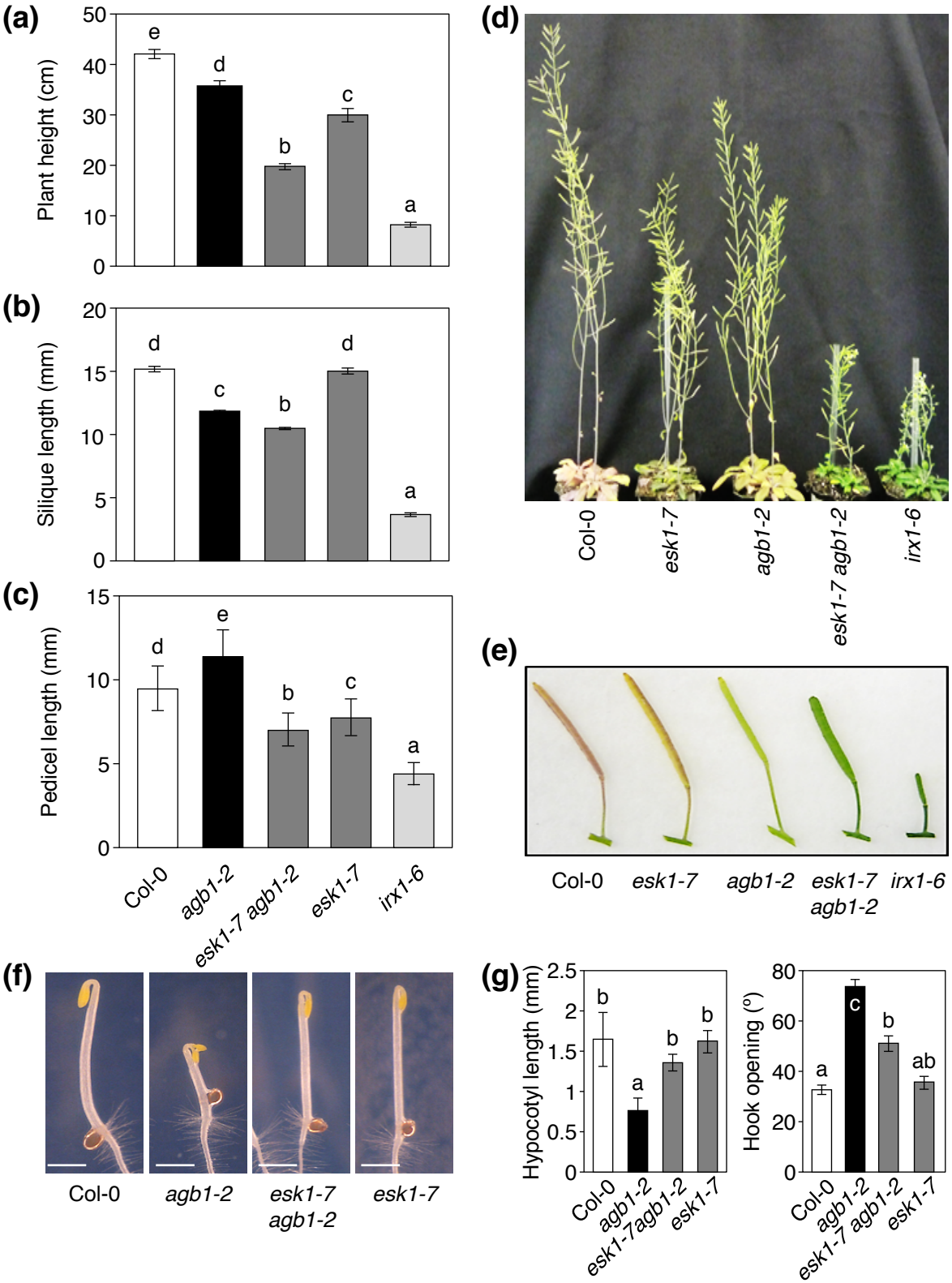


Figure S3. Morphometric analysis of *esk1-7* and *esk1-7agb1-2* plants.

Figure S3. Morphometric analysis of *esk1-7* and *esk1-7agb1-2* plants.

(a) Plant height determined in 45 day-old plants. Values are means ± SE, n = 10. (b-c) Pedicel and silique lengths from the main stem of 45 day-old plants. Values are means ± SE, n = 100. (d-e) Phenotypes of adult plants and representative siliques and pedicels from the indicated genotypes. Letters in (a), (b) and (c) indicate significantly different groups (ANOVA $p < 0.05$, Bonferroni test). Experiments were performed twice with similar results. (f) Two-day-old etiolated seedlings of the indicated genotypes. Bar, 0.5 mm. (g) Quantification of the hypocotyl lengths (mean values ± SE) and apical hook angles (mean values ± SE). At least 24 plants were analyzed. Letters indicate groups statistically different (ANOVA, $p< 0.05$, Bonferroni test).

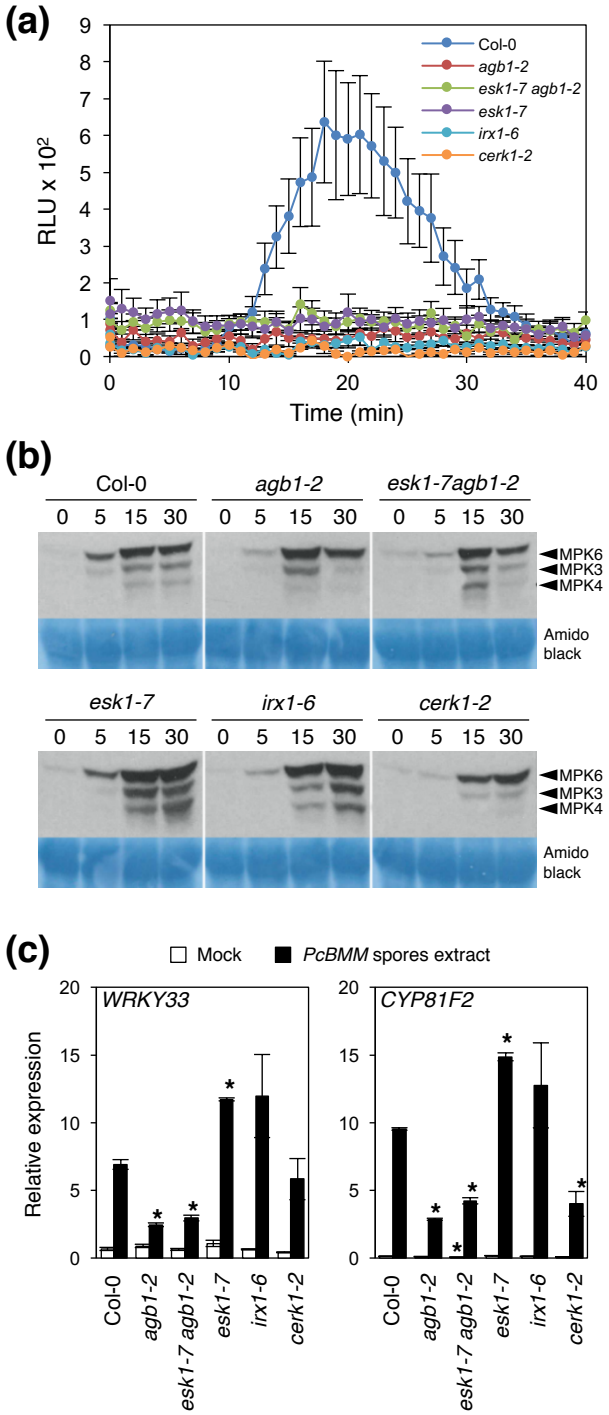


Figure S4. Early defence responses in *esk1-7* and *esk1-7 agb1-2* plants after treatment with *PcBMM* spore extract.

(a) ROS production was measured during 40 minutes after treatment of leaf discs of 21 day-old plants with the spore extract. Values (means ± SE, n = 14) are represented as relative luminescence units (RLU x 10^3). (b) MAPK phosphorylation upon application of spores extract to seedlings. Amido black-stained membranes are showed to assess equal loading. (c) qRT-PCR analyses of PTI-induced genes in mock or spore extract-treated seedling (60 min). Relative expression levels to the *UBC21* gene are shown. Values are means (± SE, n = 2). Asterisks indicate significant differences with Col-0 plants (Student's t-test, $p < 0.05$). Data are representative of three independent experiments that gave similar results.

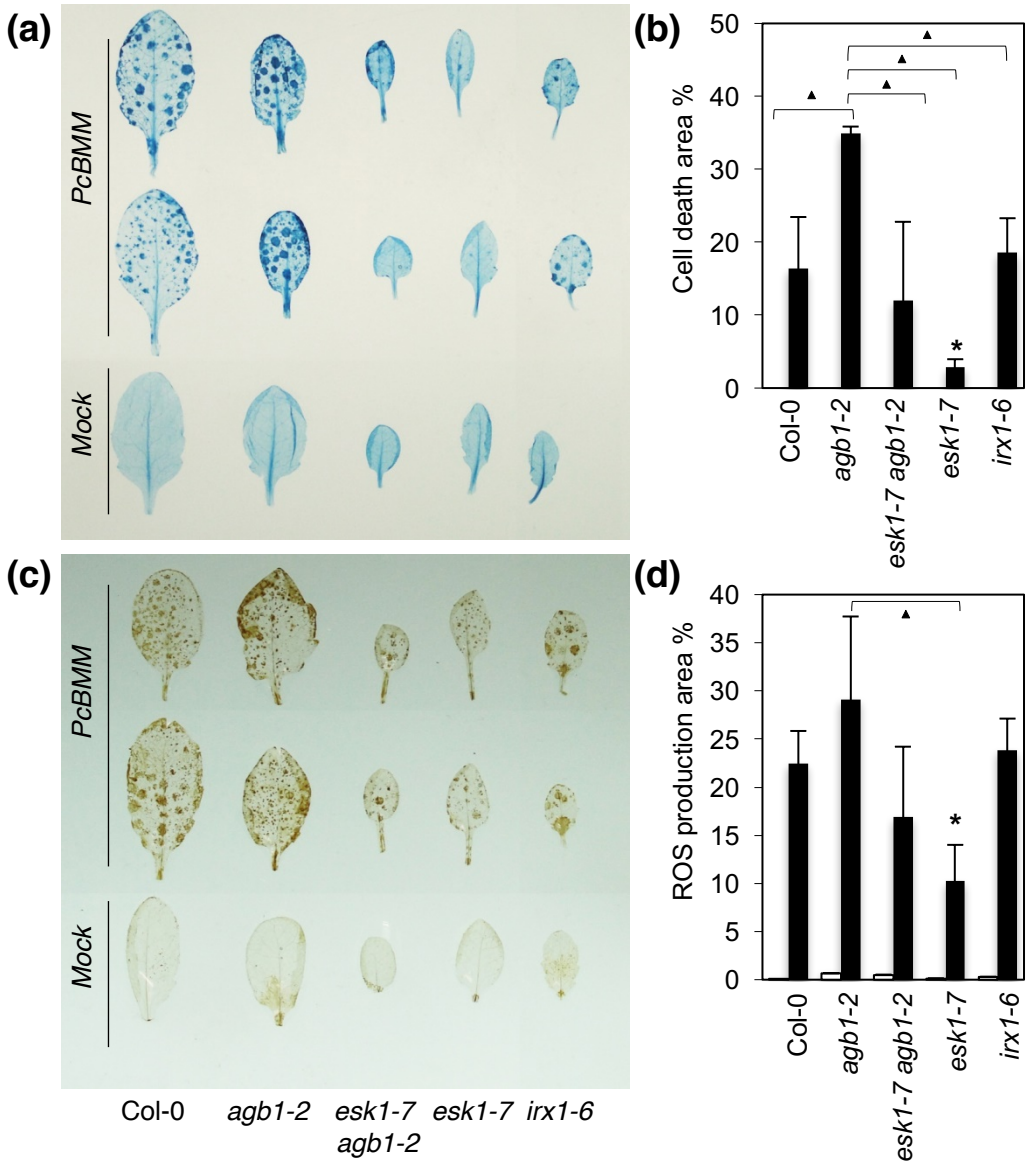


Figure S5. *esk1-7* plants show reduced cell death and ROS production upon *PcBMM* infection.

Twenty one day-old plants of the indicated genotypes were spray inoculated with a *PcBMM* suspension of 4 x 10^6 spores/ml or water (mock) and 48 hpi leaves were collected for trypan blue staining (a-b) or DAB staining (c-d). (b) and (d) Quantification of stained area from (a) and (c) was performed using Fiji software (Schindelin, *et al*., 2012). Total stained pixels were normalized to total leaf area and represented as % of total leaf surface. Black triangles indicate significant differences with *agb1-2* plants and asterisks with Col-0 plants (Student's *t*-test, $p < 0.05$).

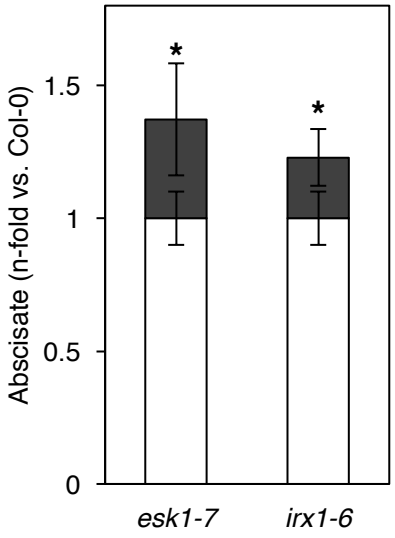


Figure S6. Abscisate levels in *esk1-7* and *irx1-6* mutants compared to Col-0 plants. Abscisate levels were measured in 25-day-old leaves of Col-0, *esk1-7* and *irx1-6* genotypes by Ultrahigh Performance Liquid Chromatography-Tandem Mass Spectroscopy (UPLC-MS/MS) with negative ion mode electrospray ionization. Values are the averages of at least three replicates form each genotype. Wild-type levels (Col-0) are indicated as the white portion of each bar and black bars indicate the portion of abscisate over accumulated in the mutants. The data are means ± SD of three replicates. Asterisks indicate statistically different from wild-type plants (Student's *t*-test, $p < 0.05$).

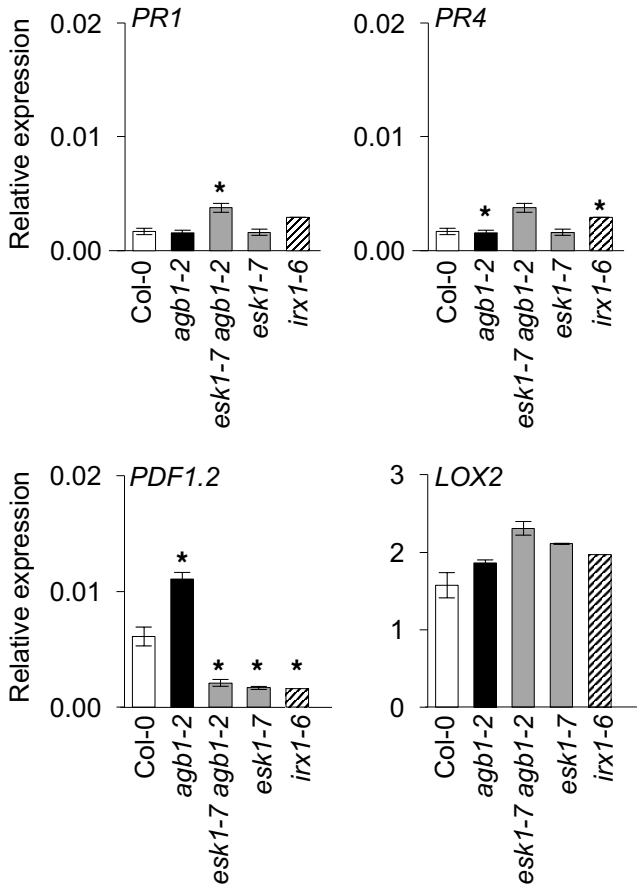


Figure S7. Expression of defense genes regulated by SA, JA and ET-mediated is not constitutively up-regulated in *esk1-7* plants.
Expression of the indicated genes was determined by qRT–PCR in tissues from 21 day-old untreated plants and their transcript levels were normalized to the Arabidopsis *UBC21* gene. Values are the average of three replicates ± SE. Asterisks indicate significant differences with Col-0 plants (Student's *t*-test, $p < 0.05$). This experiment has been performed three times with similar results.

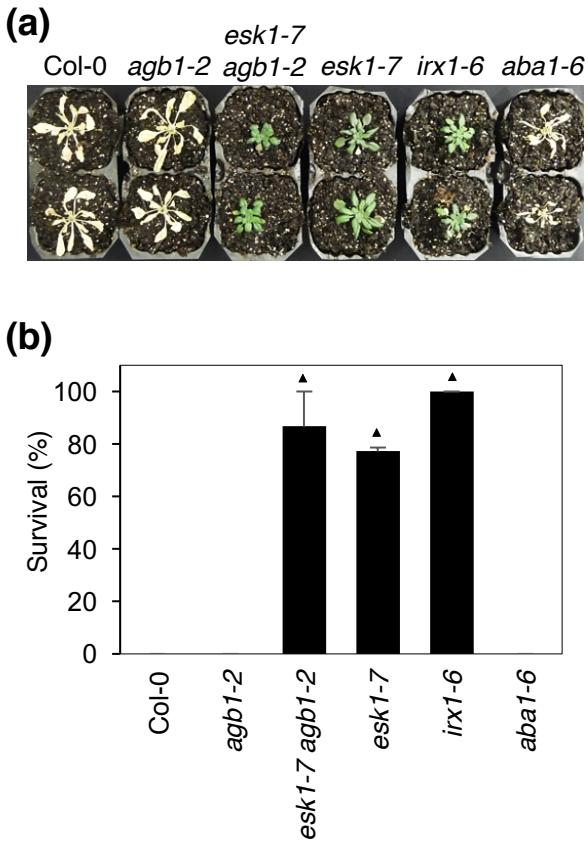


Figure S8. Response of *esk1-7* to drought stress.

(a) Drought tolerance assays with the indicated genotypes (Col-0, *agb1-2*, *esk1-7agb1-2*, *esk1-7, irx1-6* and *aba1-6*). Plants were grown in short cycle conditions for three weeks, then irrigation was limited for twenty one days and then plants were re-watered for seven days and then the macroscopic symptoms (a) were observed and the % of plants that survived (b) was determined. Data represent percentages from three independent experiments (n=24). Black triangles indicate groups statistically different from *agb1-2* and Col-0 plants (Student's *t*-test, $p < 0.05$).

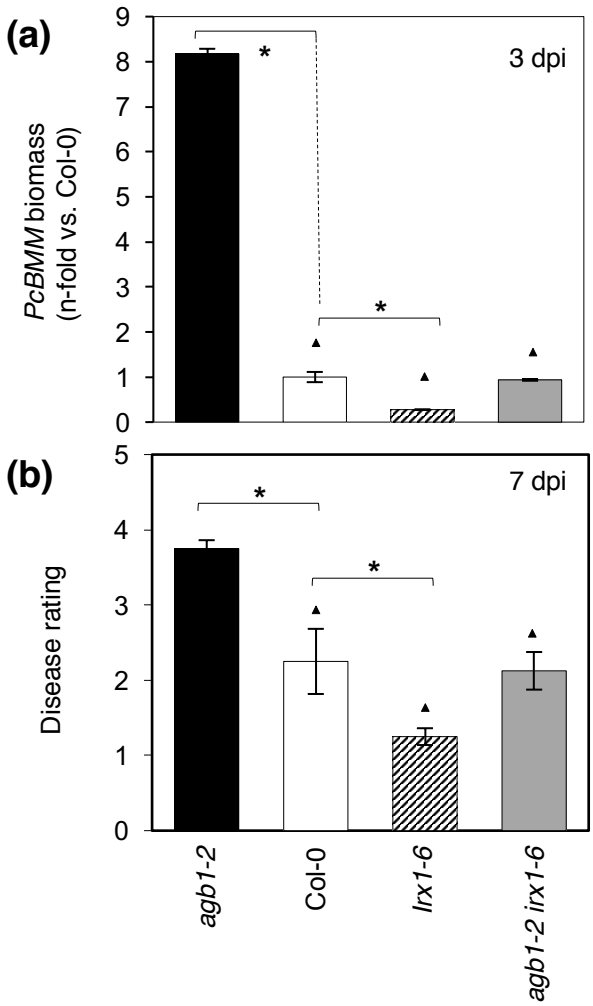


Figure S9. *Irx1-6* mutation restores the susceptibility to *PcBMM* of *agb1-2* to wild type levels.

(a) Quantification of *PcBMM* biomass in the indicated genotypes at 3 dpi. *PcBMM.* biomass was determined by qPCR analyses of *Pc β-tubulin* and Arabidopsis *UBC21* gene expression (see Experimental Procedures). Values are given as the average (± SE) of the n-fold-increase in expression compared to Col-0 plants. (b) Disease Rating scores (average values ± SE) at 7 dpi. Black triangles indicate groups statistically different from *agb1-2* and asterisks from Col-0 plants (Student's *t*-test, $p < 0.05$). These experiments have been performed three times with similar results.

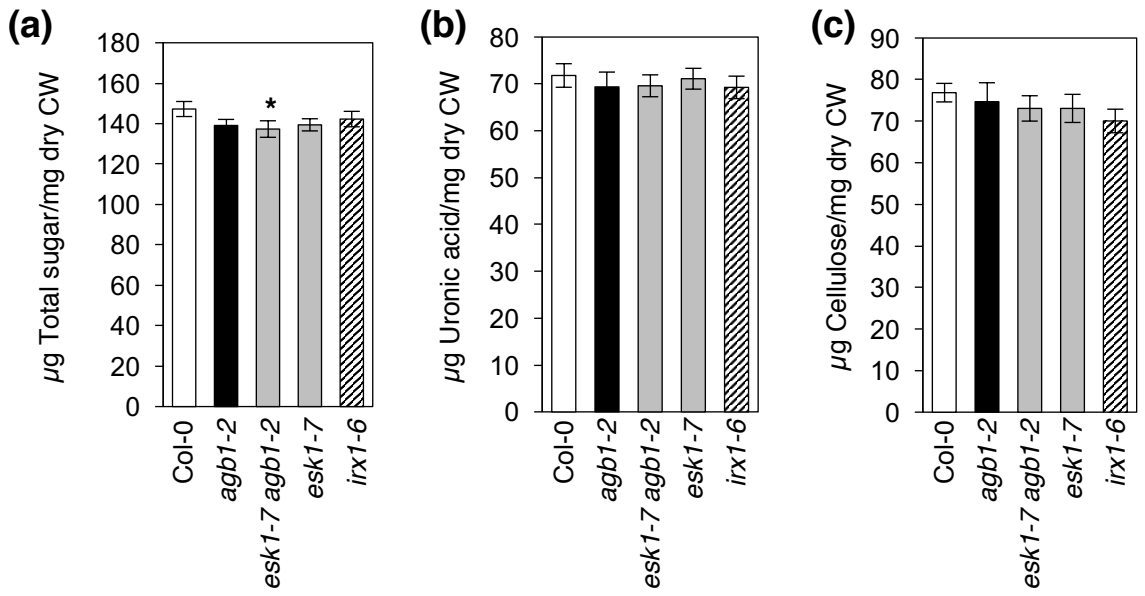
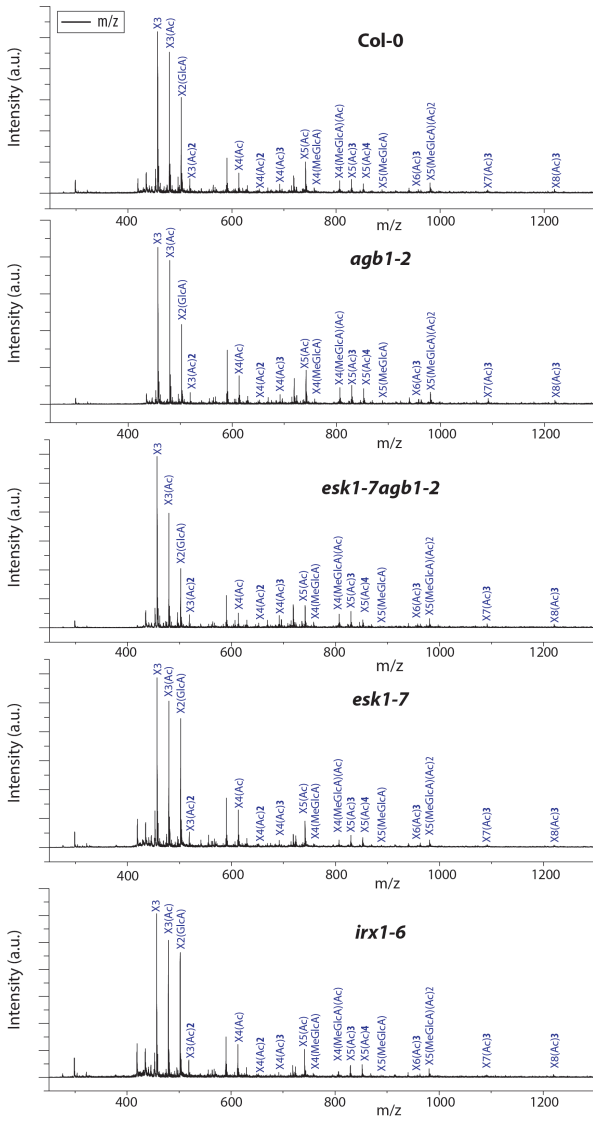


Figure S10. Biochemical composition of cell wall from Col-0, *agb1-2*, *esk1-7agb1-2*, *esk1-7* and *irx1-6* plants. (a) Quantification of total neutral sugars from the non-cellulosic carbohydrate fraction of the indicated genotypes. (b) Total uronic acid content (μg per mg of dry weight) and (c) cellulose content (μg per mg of dry weight) of the indicated genotypes. Data represent average values (± SE) of three replicates. Asterisk indicates statistically significant differences with Col-0 plants (Student's t-test, $p < 0.05$).

(a)



(b)

m/z	Oligomer
437	Xyl_3
479.6	$Xyl_3(Ac)$
502.3	$Xyl_2(GlcA)$
521	$Xyl_3(Ac)_2$
612	$Xyl_4(Ac)$
653	$Xyl_4(Ac)_2$
695	$Xyl_4(Ac)_3$
741.6	$Xyl_5(Ac)$
758.2	$Xyl_4(MeGlcA)$
806.8	$Xyl_4(MeGlcA)(Ac)$
829.6	$Xyl_5(Ac)_3$
868.9	$Xyl_5(Ac)_4$
891	$Xyl_5(MeGlcA)$
959	$Xyl_6(Ac)_3$
965	Xyl_7
980.9	$Xyl_5(MeGlcA)(Ac)_2$
1091	$Xyl_7(Ac)_3$
1223	$Xyl_8(Ac)_3$

(c)

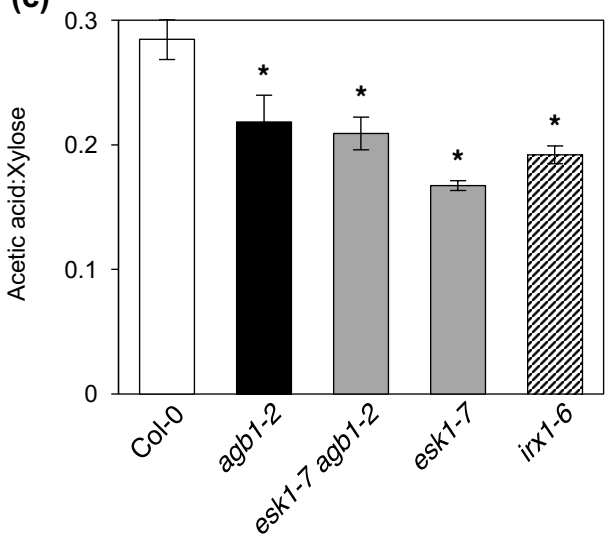


Figure S11. Xylan acetylation analysis.

(a) MALDI-TOF spectra of xylooligosaccharides generated by xylanase digestion of DMSO-extracted xylans. The data are representative of one out of three independent assays. (b) List of major ion peaks of different masses. $X_n(GlcA)_n(Ac)_n$ denote a xylo-oligomer (with n number of xylosyl residues) substituted with n number of GlcA and n number of acetyl groups. (c) Relative content of acetyl groups to xylose residues in DMSO-extracted xylans, calculated as μg mg^{-1} of fraction, from the wild type and mutants. The data are means ± SE of three independent assays.